

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 10/509,738

CRF Edit Date: 10-15-04  
Edited by: yo

Realigned nucleic acid/amino acid numbers/text in cases where the sequence  
text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

**ENTERED**

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID  
NO's edited:

Deleted: ☒ invalid beginning/end-of-file text ; ☐ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:

Revised 09/09/2003

**BEST AVAILABLE COPY**



PCT

## RAW SEQUENCE LISTING

DATE: 10/15/2004

PATENT APPLICATION: US/10/509,738

TIME: 12:23:29

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10152004\J509738.raw

3 <110> APPLICANT: Director-General of National Institute of Advanced Industrial Science and Technology; Info Genes Co., Ltd.; Kazusa DNA Research Institute

4 nce and Technology; Info Genes Co., Ltd.; Kazusa DNA Research Institute

6 <120> TITLE OF INVENTION: Application of KIAA0172 gene functions for therapeutics, diagnosis,

7 and pharmaceuticals

9 <130> FILE REFERENCE: PH-1610-PCT

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/509,738

C--> 12 <141> CURRENT FILING DATE: 2004-09-30

14 <150> PRIOR APPLICATION NUMBER: JP 2002/99422

15 <151> PRIOR FILING DATE: 2002-04-01

17 <160> NUMBER OF SEQ ID NOS: 49

19 <170> SOFTWARE: PatentIn Ver. 2.1

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 1194

23 <212> TYPE: PRT

24 <213> ORGANISM: Homo sapiens

26 <400> SEQUENCE: 1

27 Met Glu Thr Arg Arg Arg Leu Glu Gln Glu Arg Ala Thr Met Gln Met

28 1 5 10 15

30 Thr Pro Gly Glu Phe Arg Arg Pro Arg Leu Ala Ser Phe Gly Gly Met

31 20 25 30

33 Gly Thr Thr Ser Ser Leu Pro Ser Phe Val Gly Ser Gly Asn His Asn

34 35 40 45

36 Pro Ala Lys His Gln Leu Gln Asn Gly Tyr Gln Gly Asn Gly Asp Tyr

37 50 55 60

39 Gly Ser Tyr Ala Pro Ala Ala Pro Thr Thr Ser Ser Met Gly Ser Ser

40 65 70 75 80

42 Ile Arg His Ser Pro Leu Ser Ser Gly Ile Ser Thr Pro Val Thr Asn

43 85 90 95

44 Val Ser Pro Met His Leu Gln His Ile Arg Glu Gln Met Ala Ile Ala

45 100 105 110

47 Leu Lys Arg Leu Lys Glu Leu Glu Glu Gln Val Arg Thr Ile Pro Val

48 115 120 125

50 Leu Gln Val Lys Ile Ser Val Leu Gln Glu Glu Lys Arg Gln Leu Val

51 130 135 140

53 Ser Gln Leu Lys Asn Gln Arg Ala Ala Ser Gln Ile Asn Val Cys Gly

54 145 150 155 160

56 Val Arg Lys Arg Ser Tyr Ser Ala Gly Asn Ala Ser Gln Leu Glu Gln

57 165 170 175

59 Leu Ser Arg Ala Arg Arg Ser Gly Gly Glu Leu Tyr Ile Asp Tyr Glu

60 180 185 190

62 Glu Glu Glu Met Glu Thr Val Glu Gln Ser Thr Gln Arg Ile Lys Glu

63 195 200 205

65 Phe Arg Gln Leu Thr Ala Asp Met Gln Ala Leu Glu Gln Lys Ile Gln

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```

66      210      215      220
68 Asp Ser Ser Cys Glu Ala Ser Ser Glu Leu Arg Glu Asn Gly Glu Cys
69 225      230      235      240
71 Arg Ser Val Ala Val Gly Ala Glu Glu Asn Met Asn Asp Ile Val Val
72      245      250      255
73 Tyr His Arg Gly Ser Arg Ser Cys Lys Asp Ala Ala Val Gly Thr Leu
74      260      265      270
76 Val Glu Met Arg Asn Cys Gly Val Ser Val Thr Glu Ala Met Leu Gly
77      275      280      285
79 Val Met Thr Glu Ala Asp Lys Glu Ile Glu Leu Gln Gln Gln Thr Ile
80      290      295      300
82 Glu Ala Leu Lys Glu Lys Ile Tyr Arg Leu Glu Val Gln Leu Arg Glu
83 305      310      315      320
85 Thr Thr His Asp Arg Glu Met Thr Lys Leu Lys Gln Glu Leu Gln Ala
86      325      330      335
88 Ala Gly Ser Arg Lys Lys Val Asp Lys Ala Thr Met Ala Gln Pro Leu
89      340      345      350
91 Val Phe Ser Lys Val Val Glu Ala Val Val Gln Thr Arg Asp Gln Met
92      355      360      365
94 Val Gly Ser His Met Asp Leu Val Asp Thr Cys Val Gly Thr Ser Val
95      370      375      380
97 Glu Thr Asn Ser Val Gly Ile Ser Cys Gln Pro Glu Cys Lys Asn Lys
98 385      390      395      400
100 Val Val Gly Pro Glu Leu Pro Met Asn Trp Trp Ile Val Lys Glu Arg
101      405      410      415
103 Val Glu Met His Asp Arg Cys Ala Gly Arg Ser Val Glu Met Cys Asp
104      420      425      430
106 Lys Ser Val Ser Val Glu Val Ser Val Cys Glu Thr Gly Ser Asn Thr
107      435      440      445
109 Glu Glu Ser Val Asn Asp Leu Thr Leu Leu Lys Thr Asn Leu Asn Leu
110      450      455      460
112 Lys Glu Val Arg Ser Ile Gly Cys Gly Asp Cys Ser Val Asp Val Thr
113 465      470      475      480
115 Val Cys Ser Pro Lys Glu Cys Ala Ser Arg Gly Val Asn Thr Glu Ala
116      485      490      495
118 Val Ser Gln Val Glu Ala Ala Val Met Ala Val Pro Arg Thr Ala Asp
119      500      505      510
121 Gln Asp Thr Ser Thr Asp Leu Glu Gln Val His Gln Phe Thr Asn Thr
122      515      520      525
124 Glu Thr Ala Thr Leu Ile Glu Ser Cys Thr Asn Thr Cys Leu Ser Thr
125      530      535      540
127 Leu Asp Lys Gln Thr Ser Thr Gln Thr Val Glu Thr Arg Thr Val Ala
128 545      550      555      560
129 Val Gly Glu Gly Arg Val Lys Asp Ile Asn Ser Ser Thr Lys Thr Arg
130      565      570      575
132 Ser Ile Gly Val Gly Thr Leu Leu Ser Gly His Ser Gly Phe Asp Arg
133      580      585      590
135 Pro Ser Ala Val Lys Thr Lys Glu Ser Gly Val Gly Gln Ile Asn Ile
136      595      600      605

```

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```

138 Asn Asp Asn Tyr Leu Val Gly Leu Lys Met Arg Thr Ile Ala Cys Gly
139      610                      615                      620
141 Pro Pro Gln Leu Thr Val Gly Leu Thr Ala Ser Arg Arg Ser Val Gly
142 625                      630                      635                      640
144 Val Gly Asp Asp Pro Val Gly Glu Ser Leu Glu Asn Pro Gln Pro Gln
145                      645                      650                      655
147 Ala Pro Leu Gly Met Met Thr Gly Leu Asp His Tyr Ile Glu Arg Ile
148                      660                      665                      670
150 Gln Lys Leu Leu Ala Glu Gln Gln Thr Leu Leu Ala Glu Asn Tyr Ser
151                      675                      680                      685
153 Glu Leu Ala Glu Ala Phe Gly Glu Pro His Ser Gln Met Gly Ser Leu
154      690                      695                      700
156 Asn Ser Gln Leu Ile Ser Thr Leu Ser Ser Ile Asn Ser Val Met Lys
157 705                      710                      715                      720
158 Ser Ala Ser Thr Glu Leu Arg Asn Pro Asp Phe Gln Lys Thr Ser
159                      725                      730                      735
161 Leu Gly Lys Ile Thr Gly Asn Tyr Leu Gly Tyr Thr Cys Lys Cys Gly
162                      740                      745                      750
164 Gly Leu Gln Ser Gly Ser Pro Leu Ser Ser Gln Thr Ser Gln Pro Glu
165                      755                      760                      765
167 Gln Glu Val Gly Thr Ser Glu Gly Lys Pro Ile Ser Ser Leu Asp Ala
168      770                      775                      780
170 Phe Pro Thr Gln Glu Gly Thr Leu Ser Pro Val Asn Leu Thr Asp Asp
171 785                      790                      795                      800
173 Gln Ile Ala Ala Gly Leu Tyr Ala Cys Thr Asn Asn Glu Ser Thr Leu
174                      805                      810                      815
176 Lys Ser Ile Met Lys Lys Lys Asp Gly Asn Lys Asp Ser Asn Gly Ala
177                      820                      825                      830
179 Lys Lys Asn Leu Gln Phe Val Gly Ile Asn Gly Gly Tyr Glu Thr Thr
180                      835                      840                      845
182 Ser Ser Asp Asp Ser Ser Ser Asp Glu Ser Ser Ser Ser Glu Ser Asp
183      850                      855                      860
185 Asp Glu Cys Asp Val Ile Glu Tyr Pro Leu Glu Glu Glu Glu Glu
186 865                      870                      875                      880
188 Glu Asp Glu Asp Thr Arg Gly Met Ala Glu Gly His His Ala Val Asn
189                      885                      890                      895
191 Ile Glu Gly Leu Lys Ser Ala Arg Val Glu Asp Glu Met Gln Val Gln
192                      900                      905                      910
194 Glu Cys Glu Pro Glu Lys Val Glu Ile Arg Glu Arg Tyr Glu Leu Ser
195                      915                      920                      925
197 Glu Lys Met Leu Ser Ala Cys Asn Leu Leu Lys Asn Thr Ile Asn Asp
198      930                      935                      940
200 Pro Lys Ala Leu Thr Ser Lys Asp Met Arg Phe Cys Leu Asn Thr Leu
201 945                      950                      955                      960
203 Gln His Glu Trp Phe Arg Val Ser Ser Gln Lys Ser Ala Ile Pro Ala
204                      965                      970                      975
206 Met Val Gly Asp Tyr Ile Ala Ala Phe Glu Ala Ile Ser Pro Asp Val
207                      980                      985                      990
209 Leu Arg Tyr Val Ile Asn Leu Ala Asp Gly Asn Gly Asn Thr Ala Leu

```

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```

210          995          1000          1005
212 His Tyr Ser Val Ser His Ser Asn Phe Glu Ile Val Lys Leu Leu Leu
213      1010          1015          1020
214 Asp Ala Asp Val Cys Asn Val Asp His Gln Asn Lys Ala Gly Tyr Thr
215 1025          1030          1035          1040
217 Pro Ile Met Leu Ala Ala Leu Ala Ala Val Glu Ala Glu Lys Asp Met
218          1045          1050          1055
220 Arg Ile Val Glu Glu Leu Phe Gly Cys Gly Asp Val Asn Ala Lys Ala
221          1060          1065          1070
223 Ser Gln Ala Gly Gln Thr Ala Leu Met Leu Ala Val Ser His Gly Arg
224          1075          1080          1085
226 Ile Asp Met Val Lys Gly Leu Leu Ala Cys Gly Ala Asp Val Asn Ile
227      1090          1095          1100
229 Gln Asp Asp Glu Gly Ser Thr Ala Leu Met Cys Ala Ser Glu His Gly
230 1105          1110          1115          1120
232 His Val Glu Ile Val Lys Leu Leu Leu Ala Gln Pro Gly Cys Asn Gly
233          1125          1130          1135
235 His Leu Glu Asp Asn Asp Gly Ser Thr Ala Leu Ser Ile Ala Leu Glu
236          1140          1145          1150
238 Ala Gly His Lys Asp Ile Ala Val Leu Leu Tyr Ala His Val Asn Phe
239          1155          1160          1165
241 Ala Lys Ala Gln Ser Pro Gly Thr Pro Arg Leu Gly Arg Lys Thr Ser
242      1170          1175          1180
243 Pro Gly Pro Thr His Arg Gly Ser Phe Asp
244 1185          1190
247 <210> SEQ ID NO: 2
248 <211> LENGTH: 20
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
255 <400> SEQUENCE: 2
256 tactttgtgg agacccccta                                20
259 <210> SEQ ID NO: 3
260 <211> LENGTH: 21
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
267 <400> SEQUENCE: 3
268 gcttgctcgtg cccatgcctc c                                21
269 <210> SEQ ID NO: 4
270 <211> LENGTH: 20
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
277 <400> SEQUENCE: 4
278 cactggggtg gagatccctg                                20

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```

281 <210> SEQ ID NO: 5
282 <211> LENGTH: 20
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
289 <400> SEQUENCE: 5
290 attatggtag ctatgccccca 20
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 22
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
W--> 297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
300 <400> SEQUENCE: 6
301 tgcagcacat ccgcgagcag at 22
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 18
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
312 <400> SEQUENCE: 7
313 tccggcaact tacagcag 18
316 <210> SEQ ID NO: 8
317 <211> LENGTH: 20
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
324 <400> SEQUENCE: 8
325 cagctgtgag gcctcctcag 20
326 <210> SEQ ID NO: 9
327 <211> LENGTH: 22
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
334 <400> SEQUENCE: 9
335 gcctctgtgg tacacgacga tg 22
338 <210> SEQ ID NO: 10
339 <211> LENGTH: 23
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
346 <400> SEQUENCE: 10
347 aggcattctcc tgccagcctg aat 23
350 <210> SEQ ID NO: 11

```

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/509,738**

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Input Set : **A:\pto.kd.txt**Output Set: **N:\CRF4\10152004\J509738.raw**

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:297 M:283 W: Missing Blank Line separator, <220> field identifier  
L:381 M:283 W: Missing Blank Line separator, <400> field identifier  
L:495 M:283 W: Missing Blank Line separator, <220> field identifier  
L:581 M:283 W: Missing Blank Line separator, <400> field identifier  
L:635 M:283 W: Missing Blank Line separator, <220> field identifier  
L:692 M:283 W: Missing Blank Line separator, <220> field identifier  
L:778 M:283 W: Missing Blank Line separator, <400> field identifier